**EDITORIAL**

Cancer Discovery at One Year: The Editors’ Interim Analysis .... vi
Lewis C. Cantley, PhD, and José Baselga, MD, PhD, Editors-in-Chief

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**IN THIS ISSUE**

Highlighted research articles ......................... 1

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**NEWS IN BRIEF**

Important news stories affecting the community ................ 4

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**NEWS IN DEPTH**

Q&A: Craig Thompson on Research Joys and Jobs .............. 6

Jobs Wanted: Cancer Research ...................... 7

Combinations Go on Trial .............................. 8

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**RESEARCH BRIEFS**

Selected highlights of recent articles of exceptional significance from the cancer literature ...................... 9

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**ONLINE**

For more News and Research Watch, visit Cancer Discovery online at www.AACR.org/CDnews.

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**VIEWS**

In The Spotlight

A Role for ATM in Hereditary Pancreatic Cancer ............. 14
J. L. Bakker and J.P. de Winter
Commentary on Roberts et al, p. 41

Dissecting “PI3Kness”: The Complexity of Personalized Therapy for Ovarian Cancer .... 16
R. C. Bast Jr and G.B. Mills
Commentary on Honohan et al, p. 56

The 14-3-3σ Tumor Suppressor Has Multiple Functions in ErbB2-Induced Breast Cancer .... 19
N.E. Hynes and T. Smirnova
Commentary on Ling et al, p. 68

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**RESEARCH BRIEFS**

ATM Mutations in Patients with Hereditary Pancreatic Cancer ......................... 41

Précis: Next-generation sequencing identifies inherited ATM mutations in kindreds with hereditary pancreatic ductal adenocarcinoma.

Molecular Ontogeny of Donor-Derived Follicular Lymphomas Occurring after Hematopoietic Cell Transplantation ............. 47

Précis: Analysis of a donor–recipient pair with follicular lymphoma reveals the time-course of somatic mutations acquired during lymphomagenesis.

---

Tackling Formalin-Fixed, Paraffin-Embedded Tumor Tissue with Next-Generation Sequencing .................. 23
C.L. Corless and P.T. Spellman
Commentary on Wagle et al, p. 82
Genomic Complexity and AKT Dependence in Serous Ovarian Cancer .......................... 56
Précis: Individualized analyses of the PI3K/AKT and RAS pathways will identify ovarian cancers that may respond to AKT inhibition.

Loss of the 14-3-3σ Tumor Suppressor Is a Critical Event in ErbB2-Mediated Tumor Progression .......................... 68
C. Ling, V-M-T. Su, D. Zuo, and W.J. Muller
Précis: 14-3-3σ inactivation accelerates formation and promotes metastasis of ErbB2/HER2-induced tumors.

High-Throughput Detection of Actionable Genomic Alterations in Clinical Tumor Samples by Targeted, Massively Parallel Sequencing .......................... 82
Précis: Targeted, sequencing-based profiling of archival tumor samples identifies genetic alterations that can direct personalized therapy.

For more News and Research Watch, visit Cancer Discovery online at www.AACR.org/CDnews. Online-only News stories include the following:

- Biotech Firms Look for Virtual Success
- "Reversed" Krebs Cycle Can Feed Tumors
- Dual HER2 Blockade Slows Metastatic Breast Cancer
- Modified Stem Cells Create Tumor-Attacking T Cells

ON THE COVER
Wagle and colleagues describe a method to profile clinically relevant mutations in formalin-fixed, paraffin-embedded tumor samples involving exon capture of frequently mutated or polymorphic genes followed by massively parallel sequencing. This method identifies single-nucleotide variants, insertions, deletions, and copy number alterations overlooked by current genotyping-based methods with high specificity and sensitivity. Identification of such "actionable" genetic alterations that predict response to targeted or conventional cytotoxic therapies has the potential to facilitate individualized cancer treatment in a time- and cost-effective manner. For details, please see the article by Wagle and colleagues on page 82.